

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
- (ii) TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 - (B) STREET: 700 Chesterfield Village Parkway North
 - (C) CITY: St. Louis
 - (D) STATE: Missouri
 - (E) COUNTRY: USA
 - (F) ZIP: 63198
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Cohen, Charles E.
 - (B) REGISTRATION NUMBER: 34,565
 - (C) REFERENCE/DOCKET NUMBER: 38-21(10700)A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (314)537-6224
 - (B) TELEFAX: (314)537-6047

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	Leu	Cys	Glu	Arg	Pro	Ser	Gly	Thr	Xaa	Ser	Gly	Val	Cys	Gly	Asn
1				5					10					15	
Asn	Asn	Ala	Cys	Arg	Asn	Gln	Cys	Arg	Asn	Leu	Glu	Arg	Ala	Glu	His
		20					25						30		
Gly	Ser	Cys	Asn	Tyr	Val	Phe	Pro	Ala	His	Lys	Xaa	Xaa	Xaa	Tyr	Phe
		35					40						45		
Pro															

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg	Leu	Cys	Glu	Arg	Pro	Ser	Gly	Thr	Trp	Ser	Gly	Val	Cys	Gly	Asn
1				5					10					15	
Asn	Asn	Ala	Cys	Arg	Asn	Gln	Cys	Arg	Asn	Leu	Glu	Arg	Ala	Glu	His
		20					25						30		
Gly	Ser	Cys	Asn	Tyr	Val	Phe	Pro	Ala	His	Lys	Cys	Ile	Cys	Tyr	Phe
		35					40					45			
Pro Cys															
50															

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 18

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 21

(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAATTCGG ATCCACANGG NAARTARCAD ATRCA

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 18

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 19

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 23

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 24

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAATTCGG ATCGGGGNG GGNNGGGNG

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGGGGGGG GGGGGGCACA CNTCCCCTAC ACATAGATAT ACATACAAA TCACAGAAAG	60
TAATAGATAT GGCTAAGTGT GCTTCCATCA TCTCCCTTGT CTCTGCTGCT CTTGTTCTCT	120
TTGCTGCTTT TGAAGCACCA GCAATGGTGG AGTCACGGAA GTTGTGCGAG AGTCCAAGTG	180
GAACATGGTC AGGCGTGTGT GGAAACAACA ATGCTTGCAA GAATCAGTGC ATTAACCTTG	240
AAGGAGCNCG ACATGGATCT TGCAACTATG TCTTCCCAGC TCACAAGTGC ATATGCTACT	300
TCCCCTGT	308

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /d sc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: modified_bas
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGAATTCGG ATCCGTNTGY GGNAAYAAYA AYG

34

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAATTCGG ATCCTTTTTT TTTTTTTTTT TT

32

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGTGTGGGA ATAATAACGC ATGCAGGAAC CAATGCAGAA ACCTTGAAAG AGCAGAACAC

60

GGATCTTGCA ACTATGTCTT CCCAGCTCAC AAATGTATTT GTTACTTCCC ATGTTAATCT

120

ACCAAATCAC TTTTGTGCT TGTGTGTGTA TTTTACATGT TATGTGTTTA TTTACATGAA	180
ATAAGTCTGT GTCATCCTTA TGGGTGACCT TATGACATGT ACCAGATATA TCATATATGT	240
ATGTTGGTTT GTTGTGTGGC AATTATAAAC TTTTATTTGT GGATGCAAAA AAAAAAAAAA	300
AAAAAA	306

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGGGGGGG GGGGGGCACA CNTCCCCTAC ACATAGATAT ACATACAAAA TCACAGAAAG	60
TAATAGATAT GGCTAAGTGT GCTTCCATCA TCTCCCTTGT CTCTGCTGCT CTTGTTCTCT	120
TTGCTGCTTT TGAAGCACCA GCAATGGTGG AGTCACGGAA GTTGTGCGAG AGTCCAAGTG	180
GAACATGGTC AGGCGTGTGT GGAATAATA ACGCATGCAG GAACCAATGC AGAAACCTTG	240
AAAGAGCAGA ACACGGATCT TGCAACTATG TCTTCCCAGC TCACAAATGT ATTTGTTACT	300
TCCCATGTTA ATCTACCAA TCACTTTTTG TGCTTGTGTG TGTATTTTAC ATGTTATGTG	360
TTTATTTACA TGAAATAAGT CTGTGTCATC CTTATGGGTG ACCTTATGAC ATGTACCAGA	420
TATATCATAT ATGTATGTTG GTTGTGTGTG TGGCAATTAT AAACTTTTAT TTGTGGATGC	480
AAAAAAAAAA AAAAAAAAAA	500

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oth r nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGG ATCCAASAAA GTAATAGWTA TGGCTAAG

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGAATTCGG ATCCTTATTA ACATGGGAAG TAACAAATAC

40

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCGG ATCCAAGAAA GTAATAGATA TGGCTAAGTT TGCTACCATC ATCTCTCTTC	60
TCTTTGCTGC TCTTGTTCTC TTTGCTGCCT TTGAAGCACC AACAAATGGTG GATGCAAGGT	120
TGTGCGAGAG ACCAAGTGGG ACATGGTCAG GAGTTTGTGG GAACAACAAT GCATGCAGGA	180
ACCAATGCAG AAACCTTGAA AGAGCAGAAC ACGGATCTTG CAACTATGTC TTCCCAGCTC	240
ACAAATGTAT TTGTTACTTC CCATGTTAAT AAGGATCCGA ATTCCC	286

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTAGTGTTGA CCAGTGTTAC TC

22

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGATCCAASA AAGTAATAGW TATGGCTAAG TTTGCTACCA TCATCTCTCT TCTCTTTGCT	60
GCTCTTGTTT TCTTTGCTGC CTTTGAAGCA CCAACAATGG TGGATGCAAG GTTGTGCGAG	120
AGACCAAGTG GGACATGGTC AGGAGTTTGT GGGAACAACA ATGCATGCAG GAACCAATGC	180
AGAAACCTTG AAAGAGCAGA ACACGGATCT TGCAACTATG TCTTCCCAGC TCACAAATGT	240
ATTTGTTACT TCCCATGTTA ATAAGGATCC	270

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ala	Lys	Phe	Ala	Thr	Ile	Ile	Ser	Leu	Leu	Phe	Ala	Ala	Leu	Val
1				5					10					15	
Leu	Phe	Ala	Ala	Phe	Glu	Ala	Pro	Thr	Met	Val	Asp	Ala	Arg	Leu	Cys
		20						25					30		
Glu	Arg	Pro	Ser	Gly	Thr	Trp	Ser	Gly	Val	Cys	Gly	Asn	Asn	Asn	Ala
	35						40					45			
Cys	Arg	Asn	Gln	Cys	Arg	Asn	Leu	Glu	Arg	Ala	Glu	His	Gly	Ser	Cys
	50					55					60				
Asn	Tyr	Val	Phe	Pro	Ala	His	Lys	Cys	Ile	Cys	Tyr	Phe	Pro	Cys	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCCGGATCCT	CTAGAGTTTT	ATTAGTGATC	ATGGCTAAGT	TTGCGTCCAT	CATCGCACTC	60
CTCTTTGCTG	CTCTCGTTCT	CTTTGCTGCT	TTCGAGGCAC	CAACTATGGT	GGAGGCACAA	120
AAGTTGTGCG	AGAGGCCATC	AGGGACTTGG	TCAGGAGTCT	GCGGAAACAA	CAACGCATGC	180
AAGAACCAAT	GCATCAACCT	CGAGAAGGCA	CGGCATGGAT	CTTGCAACTA	CGTCTTCCCA	240
GCTCACAAGT	GCATCTGCTA	CTTTCCATGC	TAATAGGAAT	TCGAA		285

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCGGATCCT CTAGAGTTTT ATTAGTGATC ATGGCTAAGT TTGCGTCCAT CATCGCACTC	60
CTCTTTGCTG CTCTCGTTCT CTTTGCTGCT TTCGAGGCAC CAACTATGGT GGAGGCACAA	120
AAGTTGTGCC AAAGGCCATC AGGGACTTGG TCAGGAGTCT GCGGAAACAA CAACGCATGC	180
AAGAACCAAT GCATCAGACT CGAGAAGGCA CGGCATGGAT CTTGCAACTA CGTCTTCCCA	240
GCTCACAAGT GCATCTGCTA CTTTCCATGC TAATAGGAAT TCGAA	285

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln	Lys	Leu	Cys	Glu	Arg	Pro	Ser	Gly	Thr	Trp	Ser	Gly	Val	Cys	Gly
1			5					10					15		
Asn	Asn	Asn	Ala	Cys	Lys	Asn	Gln	Cys	Ile	Asn	Leu	Glu	Lys	Ala	Arg
			20					25					30		
His	Gly	Ser	Cys	Asn	Tyr	Val	Phe	Pro	Ala	His	Lys	Cys	Ile	Cys	Tyr
			35					40					45		
Phe	Pro	Cys													
			50												

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln	Lys	Leu	Cys	Gln	Arg	Pro	Ser	Gly	Thr	Trp	Ser	Gly	Val	Cys	Gly
1			5					10					15		

Asn	Asn	Asn	Ala	Cys	Lys	Asn	Gln	Cys	Ile	Arg	Leu	Glu	Lys	Ala	Arg
			20				25						30		

His	Gly	Ser	Cys	Asn	Tyr	Val	Phe	Pro	Ala	His	Lys	Cys	Ile	Cys	Tyr
	35						40					45			

Phe	Pro	Cys
	50	